

SEQUENCE LISTING

<110> Consiglio Nazionale delle Ricerche

5 <120> Fusion proteins

<130> BW352R

<160> 7

<170> PatentIn version 3.2

10 <210> 1

<211> 732

<212> DNA

<213> Parietaria judaica

<222> (1)..(729)

15 <220>

<221> misc_feature

<222> (10)..(12); (40)..(42); (85)..(90); (148)..(150); (154)..(156);
(271)..(273); (322)..(324); (352)..(354); (397)..(402); (460)..(462);
(466)..(468); (535)..(537); (583)..(585)

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25 gag gag gct nnn ggg aaa gtg gtg cag gat ata atg ccg nnn ctg cat 48

Glu Glu Ala Xaa Gly Lys Val Val Gln Asp Ile Met Pro Xaa Leu His

1 5 10 15

30 ttc gtg aag ggg gag gag aag gag ccg tcg aag gag nnn nnn agc ggc 96

Phe Val Lys Gly Glu Lys Glu Pro Ser Lys Glu Xaa Xaa Ser Gly

20 25 30

35 acg aag aag ctg agc gag gag gtg aag acg acg gag cag aag agg gag 144

Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu

35 40 45

45 gcc nnn aag nnn ata gtg cgc gcc acg aag ggc atc tcc ggt atc aaa 192

Ala Xaa Lys Xaa Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys

50 55 60

50 aat gaa ctt gtc gcc gag gtc ccc aag aag nnn gat att aag acc act 240

Asn Glu Leu Val Ala Glu Val Pro Lys Xaa Asp Ile Lys Thr Thr

65 70 75 80

45 ctc ccg ccc atc acc gcc gac ttc gac tgc nnn aag atc caa agt act 288

Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Xaa Lys Ile Gln Ser Thr

85 90 95

att ttc aga ggt tac tat gga ttc caa gaa acc nnn ggg act atg gtg 336

Ile Phe Arg Gly Tyr Tyr Gly Phe Gln Glu Thr Xaa Gly Thr Met Val

100 105 110

aga gcg ctg atg ccg nnn ctg ccg ttc gtg cag ggg aaa gag aaa gag 384
 Arg Ala Leu Met Pro Xaa Leu Pro Phe Val Gln Gly Lys Glu Lys Glu
 115 120 125

5 ccg tca aag ggg nnn nnn agc ggc gcc aaa aga ttg gac ggg gag acg 432
 Pro Ser Lys Gly Xaa Xaa Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr
 130 135 140

10 aag acg ggg ccg cag agg gtg cac gct nnn gag nnn atc cag acc gcc 480
 Lys Thr Gly Pro Gln Arg Val His Ala Xaa Glu Xaa Ile Gln Thr Ala
 145 150 155 160

15 atg aag act tat tcc gac atc gac ggg aaa ctc gtc agc gag gtc ccc 528
 Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro
 165 170 175

20 aag cac nnn ggc atc gtt gac agc aag ctc ccg ccc att gac gtc aac 576
 Lys His Xaa Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn
 180 185 190

25 atg gac nnn aag aca gtt gga gtg gtt cct cgg caa ccc ctt cca 624
 Met Asp Xaa Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro
 195 200 205

30 gtc tct ctc cgt cat ggt ccc gtc acg ggc cca agt gat ccc gcc cac 672
 Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His
 210 215 220

35 aaa gca cgg ttg gag aga ccc cag att aga gtt ccg ccc ccc gca ccg 720
 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Ala Pro
 225 230 235 240

gaa aaa gcc taa 732
 Glu Lys Ala

40 <210> 2
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 <212> PRT
 <213> Parietaria judaica

45 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The 'Xaa' at location 4, 14, 29, 30, 50, 52, 75, 91, 108, 118, 133,
 154, 156, 179, 195 stands for Asn, Ser, Thr, Ile, Met, Gly, Ala, Val, Gln or
 Leu.

50 <400> 2

Glu Glu Ala Xaa Gly Lys Val Val Gln Asp Ile Met Pro Xaa Leu His
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5 Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Xaa Xaa Ser Gly
20 25 30

Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu
35 40 45

10 Ala Xaa Lys Xaa Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys
50 55 60

15 Asn Glu Leu Val Ala Glu Val Pro Lys Lys Xaa Asp Ile Lys Thr Thr
65 70 75 80

Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Xaa Lys Ile Gln Ser Thr
85 90 95

20 Ile Phe Arg Gly Tyr Tyr Gly Phe Gln Glu Thr Xaa Gly Thr Met Val
100 105 110

Arg Ala Leu Met Pro Xaa Leu Pro Phe Val Gln Gly Lys Glu Lys Glu
115 120 125

25 Pro Ser Lys Gly Xaa Xaa Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr
130 135 140

Lys Thr Gly Pro Gln Arg Val His Ala Xaa Glu Xaa Ile Gln Thr Ala
30 145 150 155 160

Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro
165 170 175

35 Lys His Xaa Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn
180 185 190

40 Met Asp Xaa Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro
195 200 205

Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His
210 215 220

45 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Pro Ala Pro
225 230 235 240

50 Glu Lys Ala

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1	5	10		
		15		
15	ttc gtg aag ggg gag gag aag gag ccg tcg aag gag agc agc agc ggc	96		
	Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Ser Ser Ser Gly			
	20	25	30	
20	acg aag aag ctg agc gag gag gtg aag acg acg gag cag aag agg gag	144		
	Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu			
	35	40	45	
25	gcc tgc aag tgc ata gtg cgc gcc acg aag ggc atc tcc ggt atc aaa	192		
	Ala Cys Lys Cys Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys			
	50	55	60	
30	aat gaa ctt gtc gcc gag gtc ccc aag aag tgc gat att aag acc act	240		
	Asn Glu Leu Val Ala Glu Val Pro Lys Lys Cys Asp Ile Lys Thr Thr			
	65	70	75	80
35	ctc ccg ccc atc acc gcc gac ttc gac tgc tcc aag atc caa agt act	288		
	Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Ser Lys Ile Gln Ser Thr			
	85	90	95	
40	att ttc aga ggt tac tat gga ttc caa gaa acc agc ggg act atg gtg	336		
	Ile Phe Arg Gly Tyr Tyr Gly Phe Gln Glu Thr Ser Gly Thr Met Val			
	100	105	110	
45	aga gcg ctg atg ccg tgc ctg ccg ttc gtg cag ggg aaa gag aaa gag	384		
	Arg Ala Leu Met Pro Cys Leu Pro Phe Val Gln Gly Lys Glu Lys Glu			
	115	120	125	
50	ccg tca aag ggg agc agc agc ggc gcc aaa aga ttg gac ggg gag acg	432		
	Pro Ser Lys Gly Ser Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr			
	130	135	140	
55	aag acg ggg ccg cag agg gtg cac gct tgt gag tgc atc cag acc gcc	480		
	Lys Thr Gly Pro Gln Arg Val His Ala Cys Glu Cys Ile Gln Thr Ala			
	145	150	155	160
60	atg aag act tat tcc gac atc gac ggg aaa ctc gtc agc gag gtc ccc	528		
	Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro			
	165	170	175	

aag cac tgc ggc atc gtt gac agc aag ctc ccg ccc att gac gtc aac 576
 Lys His Cys Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn
 180 185 190

5 atg gac tgc aag aca gtt gga gtg gtt cct cgg caa ccc caa ctt cca 624
 Met Asp Cys Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro
 195 200 205

10 gtc tct ctc cgt cat ggt ccc gtc acg ggc cca agt gat ccc gcc cac 672
 Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His
 210 215 220

15 aaa gca cgg ttg gag aga ccc cag att aga gtt ccg ccc ccc gca ccg 720
 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Ala Pro
 225 230 235 240

20 gaa aaa gcc taa 732
 Glu Lys Ala

25 <210> 4
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 Glu Glu Ala Ser Gly Lys Val Val Gln Asp Ile Met Pro Cys Leu His
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35 Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Ser Ser Ser Gly
 20 25 30

40 Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu
 35 40 45

Ala Cys Lys Cys Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys
 50 55 60

45 Asn Glu Leu Val Ala Glu Val Pro Lys Lys Cys Asp Ile Lys Thr Thr
 65 70 75 80

Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Ser Lys Ile Gln Ser Thr
 85 90 95

Ile Phe Arg Gly Tyr Tyr Gly Phe Gln Glu Thr Ser Gly Thr Met Val
 100 105 110

50 Arg Ala Leu Met Pro Cys Leu Pro Phe Val Gln Gly Lys Glu Lys Glu
 115 120 125

Pro Ser Lys Gly Ser Ser Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr
130 135 140

5 Lys Thr Gly Pro Gln Arg Val His Ala Cys Glu Cys Ile Gln Thr Ala
145 150 155 160

Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro
10 165 170 175

10 Lys His Cys Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn
180 185 190

Met Asp Cys Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro
15 195 200 205

15 Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His
210 215 220

20 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Pro Ala Pro
225 230 235 240

Glu Lys Ala

25 <210> 5
<211> 18
<212> DNA
<213> Artificial

30 <220>
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35 <210> 6
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<212> DNA
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40 <220>
<223> forward primer for insertion of mutation in position 4

<400> 6
45 gtgggatccg aggaggctag cggaaaagtg 30

<210> 7
<211> 24
<212> DNA
50 <213> Artificial

<220>

<223> reverse parj2 primer

<400> 7

5 gggggatcca tagtaacctc tgaa

24